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OM protein - protein search, using sw model

Run on: June 25, 2003, 14:20:45 ; Search time 5.71318 Seconds

(Without alignments)  
798.574 Million cell updates/sec

Title: US-09-622-613B-15

Perfect score: 602

Sequence: 1 QMWFQOKHIIITPICNT.....ICVKGCEQYVPHFAGIGRCP 110

Scoring table: BL0SUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	591.5	98.3	111	1	RNPO_RANCA
2	455	75.6	111	1	IECS_RANCA
3	374	62.1	111	1	RNPE_RANCA
4	277.5	46.1	104	1	RN30_RANPI
5	154.5	25.7	145	1	ANG3_MOUSE
6	149.5	24.8	145	1	ANGR_MOUSE
7	135.5	22.5	124	1	RNP_BALAC
8	135.5	22.5	145	1	ANGI_MOUSE
9	133.5	22.2	167	1	RNBR_BOVIN
10	132.5	22.0	124	1	RNP_PIG
11	131.5	21.8	119	1	RNP_IGUG
12	128.5	21.3	151	1	RNBR_CARCA
13	127.5	21.2	123	1	ANG2_BOVIN
14	127.5	21.2	141	1	RNBR_GIRCA
15	127.5	21.2	151	1	RNBR_AXIPR
16	125	20.8	146	1	ANGI_SAISC
17	124	20.6	146	1	ANGI_MIOGA
18	123.5	20.5	143	1	RNBR_SHEEP
19	122.5	20.3	124	1	RNP_ANTMA
20	122.5	20.3	146	1	ANGI_CERAE
21	122	20.3	122	1	RNP_MACRO
22	120.5	20.0	138	1	RNP_MYOCO
23	120.5	20.0	149	1	RNP_MOUSE
24	120	19.9	146	1	ANGI_AOTTR
25	120	19.9	147	1	ANGI_PONPY
26	119.5	19.9	123	1	ANGI_PIG
27	118.5	19.7	128	1	RNPE_CAVPO
28	118	19.6	146	1	ANGI_SAGOE
29	117.5	19.5	128	1	RNP_HORSE
30	116.5	19.4	124	1	RNP_CAMDR
31	116.5	19.4	128	1	RNP_PROCU
32	115.5	19.2	146	1	ANGI_MACMU
33	114	18.9	148	1	ANGI_BOVIN

## ALIGNMENTS

RESULT 1	RNPO_RANCA	STANDARD:	PRT:	111 AA.
AC	P11916:			
DT	01-OCT-1989 (Rel. 12, Created)			
DT	01-FEB-1994 (Rel. 28, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Ribonuclease, oocytes (EC 3.1.27.-) (RC-RNase) (Sialic acid-binding lectin) (SBL-C).			
OS	Rana catesbeiana (bull frog).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana.			
OX	NCBI_Taxid=8400;			
RN	[1]			
RP	SEQUENCE.			
RC	TISSUE=Egg;			
RX	MEDLINE=87299649; PubMed=3304421;			
RA	Tilani K., Takio K., Kwada M., Nitta K., Sakakibara F., Kawachi H.,			
RA	Takayanagi G., Hakomori S.;			
RT	"Amino acid sequence of sialic acid binding lectin from frog (Rana			
RT	catesbeiana) oocytes.";			
RL	Biochemistry 26:2189-2194(1987).			
RN	[2]			
RP	CHARACTERIZATION, AND SEQUENCE OF 59-79.			
RX	MEDLINE=92220613; PubMed=1373237;			
RA	Liao Y.-D.;			
RT	"A pyrimidine-guanine sequence-specific ribonuclease from Rana			
RT	catesbeiana (bullfrog) oocytes.";			
RL	Nucleic Acids Res. 20:1371-1377(1992).			
RN	[3]			
RP	CHARACTERIZATION.			
RC	TISSUE=Egg;			
RX	MEDLINE=93192604; PubMed=8448385;			
RA	Nitta K., Oyama F., Sekiguchi K., Kawachi H.,			
RA	Takayanagi Y., Hakomori S., Tilani K.;			
RT	"Ribonuclease activity of sialic acid-binding lectin from Rana			
RT	catesbeiana eggs.";			
RL	Glycobiology 3:37-45(1993).			
RN	[4]			
RP	STRUCTURE BY NMR.			
RX	MEDLINE=96437383; PubMed=9761686;			
RA	Chang C.-F., Chen C., Chen Y.-C., Hom K., Huang R.-F., Huang T.H.;			
RT	"The solution structure of a cytotoxic ribonuclease from the oocytes			
RT	of Rana catesbeiana (bullfrog).";			
RL	J. Mol. Biol. 283:231-244(1998).			
CC	-1- FUNCTION: PREFERENTIALLY CLEAVES SINGLE-STRANDED RNA AT PYRIMIDINE			
CC	RESIDUES WITH A 3' FLANKING GUANINE. HYDROLYSES POLY(U) AND POLY(C)			
CC	AS SUBSTRATES, AND PREFERENCES THE FORMER. THE S-LECTIN IN FROG EGGS			
CC	MAY BE INVOLVED IN THE FERTILIZATION AND DEVELOPMENT OF THE FROG			
CC	EMBRYO. THIS LECTIN AGGLUTINATES VARIOUS ANIMAL CELLS, INCLUDING			
CC	NORMAL LYMPHOCYTES, ERYTHROCYTES, AND FIBROBLASTS OF ANIMAL AND			
CC	HUMAN ORIGIN.			
CC	-1- SUBUNIT: MONOMER.			
CC	-1- SUBCELLULAR LOCATION: Secreted.			
CC	-1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.			
CC	PIR: A27121; A27121.			

34	113.5	18.9	124	1	RNP_RANCA	P00666	rangifer ta
35	113.5	18.9	146	1	ANGI_PAPHA	Q8wn64	papio hamad
36	113	18.8	147	1	ANGI_HUMAN	P03950	homo sapien
37	113	18.8	147	1	ANGI_PANTR	Q8wn68	pan troglod
38	112.5	18.7	124	1	RNP_CARCA	P00664	capreolus c
39	112.5	18.7	148	1	RNP_GIRCA	Q9j3h1	giraffa cam
40	112.5	18.7	148	1	RNL4_MOUSE	P00662	mus musculu
41	112	18.6	125	1	ANGI_RABIT	P31347	oryctolagus
42	111.5	18.5	130	1	RNP_CRITO	P24717	cricetus
43	111.5	18.5	147	1	RNL4_RAT	O55004	rattus norv
44	111.5	18.5	149	1	RNP_ACOCA	Q9wt55	acomys cahi
45	110.5	18.4	124	1	RNP_AEPME	P07847	aepyrocero m

PDB: 1BC4; 28-OCT-98.  
 DR InterPro: IPR001427; RNaseA.  
 DR Pfam: PF00074; RNaseA; 1.  
 DR ProDom: PD000535; RNaseA; 1.  
 DR SMART: SM00092; RNase\_Pc; 1.  
 DR PROSITE: PS00127; RNASE\_PANCREATIC; 1.  
 DR Hydrolyase: Nuclease; Endonuclease; Sialic acid; Lectin; 3D-structure.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT ACT\_SITE 10 10  
 FT ACT\_SITE 35 35  
 FT ACT\_SITE 103 103  
 FT DISULFID 19 71  
 FT DISULFID 34 81  
 FT DISULFID 52 96  
 FT DISULFID 93 110  
 SQ SEQUENCE 111 AA; 12464 MW; 0BC9E5F55729ECFA CRC64;

Query Match 98.3%; Score 591.5; DB 1; Length 111;  
 Best Local Similarity 99.1%; Pred. No. 4.2e-57;  
 Matches 110; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 1 QNMAFPQOKHINPPI-CNTIMDNNTIYVGGCKRVNFTFISSATTVKATCTGVINNV 59  
 DB 1 QNMAFPQOKHINPPIINNTIMDNNTIYVGGCKRVNFTFISSATTVKATCTGVINNV 60

OY 60 LSTTRFOLNCTRTSTTPPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110  
 DB 61 LSTTRFOLNCTRTSTTPPCPYSSRTETNYICVKCENQYPVHFAGIGRC 111

RESULT 2  
 LECS\_RANCA STANDARD; PRT; 111 AA.  
 ID LECS\_RANCA  
 AC P18839;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Sialic acid-binding lectin (EC 3.1.27.-)  
 OS Rana japonica (Japanese reddish frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.  
 NX NCBI\_TaxID=8402;  
 RN [1]  
 RP SEQUENCE, AND DISULFIDE BONDS.  
 RC TISSUE-Egg;  
 RX MEDLINE=9103319; PubMed=2229005;  
 RA Kaniya Y., Oyama F., Oyama R., Sakakibara F., Nitta K., Kawachi H.,  
 RT Takayanagi Y., Titani K.;  
 RT "Amino acid sequence of a lectin from Japanese frog (Rana japonica) eggs."  
 RL J. Biochem. 108:139-143(1990).  
 CC -1- FUNCTION: THE S-LECTINS IN FROG EGGS MAY BE INVOLVED IN THE  
 CC FERTILIZATION AND DEVELOPMENT OF THE FROG EMBRYO. THIS LECTIN  
 CC PREFERENTIALLY AGGLUTININATE A LARGE VARIETY OF TUMOR CELLS, BUT IT  
 CC DOES NOT AGGLUTININATE NON-TRANSFORMED CELLS AND ERYTHROCYTES.  
 CC -1- SUBUNIT: MONOMER.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.  
 DR HSP: P11916; 1BC4.  
 DR InterPro: IPR001427; RNaseA.  
 DR Pfam: PF00074; RNaseA; 1.  
 DR ProDom: PD000535; RNaseA; 1.  
 DR SMART: SM00092; RNase\_Pc; 1.  
 DR PROSITE: PS00127; RNASE\_PANCREATIC; 1.  
 KM Hydrolyase: Nuclease; Endonuclease; Sialic acid; Lectin.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT ACT\_SITE 10 10  
 FT ACT\_SITE 35 35  
 FT ACT\_SITE 103 103  
 FT DISULFID 19 72  
 FT DISULFID 34 82  
 FT DISULFID 52 97

FT DISULFID 94 111  
 SQ SEQUENCE 111 AA; 12326 MW; FDEBDDF3834ED679 CRC64;

Query Match 75.6%; Score 455; DB 1; Length 111;  
 Best Local Similarity 78.4%; Pred. No. 2.2e-47;  
 Matches 87; Conservative 7; Mismatches 15; Indels 2; Gaps 2;

OY 1 QNMAFPQOKHINPPI-ICNTIMDNNTIYVGGCKRVNFTFISSATTVKATCTGVINNV 58  
 DB 1 QNMAFPQOKHINPPIINNTIMDNNTIYVGGCKRVNFTFISSATTVKATCTGVINNV 60

OY 59 VLSTTRFOLNCTRTSTTPPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109  
 DB 61 VLSTTRFOLNCTRTSTTPPCPYSSRTETNYICVKCENQYPVHFAGIGRC 111

RESULT 3  
 RNPL\_RANCA STANDARD; PRT; 111 AA.  
 ID RNPL\_RANCA  
 AC P14626;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Ribonuclease, liver (EC 3.1.27.5).  
 OS Rana catesbeiana (Bull frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.  
 NX NCBI\_TaxID=8400;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE-Liver;  
 RX MEDLINE=90130374; PubMed=2613682;  
 RA Nitta R., Katayama N., Okabe Y., Iwama M., Watanabe H., Abe Y.,  
 RT Okazaki T., Ohgi K., Irie M.;  
 RT "Primary structure of a ribonuclease from bullfrog (Rana catesbeiana) liver."  
 RL J. Biochem. 106:729-735(1989).  
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-  
 CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P  
 CC with 2',3'-cyclic phosphate intermediates.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.  
 DR PIR: JX0085; JX0085.  
 DR HSP: P11916; 1BC4.  
 DR InterPro: IPR001427; RNaseA.  
 DR Pfam: PF00074; RNaseA; 1.  
 DR ProDom: PD000535; RNaseA; 1.  
 DR SMART: SM00092; RNase\_Pc; 1.  
 DR PROSITE: PS00127; RNASE\_PANCREATIC; 1.  
 KM Hydrolyase: Nuclease; Endonuclease.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT ACT\_SITE 10 10  
 FT ACT\_SITE 35 35  
 FT ACT\_SITE 104 104  
 FT ACT\_SITE 19 72  
 FT DISULFID 34 82  
 FT DISULFID 52 97  
 FT DISULFID 94 111  
 SQ SEQUENCE 111 AA; 12461 MW; D64BA72456C10788 CRC64;

Query Match 62.1%; Score 374; DB 1; Length 111;  
 Best Local Similarity 65.8%; Pred. No. 1.2e-33;  
 Matches 73; Conservative 9; Mismatches 27; Indels 2; Gaps 2;

OY 1 QNMAFPQOKHINPPI-CNTIMDNNTIYVGGCKRVNFTFISSATTVKATCTGVINNV 58  
 DB 1 QNMAFPQOKHINPPIINNTIMDNNTIYVGGCKRVNFTFISSATTVKATCTGVINNV 60

OY 59 VLSTTRFOLNCTRTSTTPPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109  
 DB 61 ELSTTRFOLNCTRTSTTPPCPYSSRTETNYICVKCENQYPVHFAGIGRC 111

RESULT 4  
 RN30\_RANPI STANDARD: PRT: 104 AA.  
 AC P22069;  
 DT 01-AUG-1991 (Rel. 19, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 01-FEB-1995 (Rel. 31, Last annotation update)  
 DE P-30 protein (EC 3.1.27.-) (onconase).  
 OS Rana pipiens (Northern leopard frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.  
 OX NCBI\_TaxID=8404;  
 RN [1]  
 RC SEQUENCE.  
 RP TISSUE=Embryo;  
 RX MEDLINE=91093131; PubMed=1985696;  
 RA Ardelt W., Mikulski S.M., Shogen K.;  
 RT "Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and early embryos. Homology to pancreatic ribonucleases.";  
 RL J. Biol. Chem. 266:245-251(1991).  
 RN [2]  
 RP 3D-STRUCTURE MODELING.  
 RX MEDLINE=93066156; PubMed=1438177;  
 RA Mosmann S.C., Johns K.L., Ardelt W., Mikulski S.M., Shogen K., James M.N.G.;  
 RT "Comparative molecular modeling and crystallization of P-30 protein: a novel anti-tumor protein of Rana pipiens oocytes and early embryos.";  
 RL Proteins 14:392-400(1992).  
 RN [3]  
 RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).  
 RX MEDLINE=94166079; PubMed=8120892;  
 RA Mosmann S.C., Ardelt W., James M.N.G.;  
 RT "Refined 1.7 A x-ray crystallographic structure of P-30 protein, an amphibian ribonuclease with anti-tumor activity.";  
 RL J. Mol. Biol. 236:1141-1153(1994).  
 CC -1- FUNCTION: BASIC PROTEIN WITH ANTI-PROLIFERATIVE/CYTOTOXIC ACTIVITY IN VIVO. IT EXHIBITS A RIBONUCLEASE-LIKE ACTIVITY AGAINST HIGH MOLECULAR WEIGHT RIBOSOMAL RNA.  
 CC -1- DEVELOPMENTAL STAGE: EARLY EMBRYOS (UP TO FOUR BLASTOMERE STAGE).  
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.  
 CC PDB: 1ONC; 31-JAN-94.  
 DR InterPro: IPR001427; Rnasea.  
 DR Pfam: PF00074; rnaasea.1.  
 DR ProDom: PD006535; Rnasea.1.  
 DR SMART: SM00052; Rnase\_Pc.1.  
 DR PROSITE: PS00127; Rnase\_Pancreatic.1.  
 KW Hydrolase; Nuclease; Endonuclease; 3D-structure.  
 FT MOD\_RES 1  
 FT ACT\_SITE 10  
 FT ACT\_SITE 31  
 FT ACT\_SITE 97  
 FT DISULFID 19  
 FT DISULFID 30  
 FT DISULFID 75  
 FT DISULFID 87  
 FT DISULFID 104  
 FT HELIX 3  
 FT STRAND 10  
 FT STRAND 11  
 FT HELIX 12  
 FT HELIX 19  
 FT TURN 22  
 FT TURN 23  
 FT TURN 24  
 FT TURN 30  
 FT STRAND 33  
 FT STRAND 38  
 FT STRAND 41  
 FT HELIX 48  
 FT TURN 49  
 FT TURN 50  
 FT STRAND 55  
 FT STRAND 58  
 FT TURN 63  
 FT TURN 70  
 FT TURN 74  
 FT STRAND 77  
 FT STRAND 84  
 FT TURN 86  
 FT TURN 91  
 FT TURN 92  
 FT TURN 93  
 FT STRAND 94  
 FT STRAND 101  
 SQ SEQUENCE 104 AA; 11845 MW; 22A753C2P9E566B4 CRC64;

Query Match 46.1%; Score 277.5; DB 1; Length 104;  
 Best Local Similarity 49.5%; Pred. No. 2,9e-23;  
 Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;  
 QY 1 QNATFQOKHIIINT-PICTNTMDNNIYVGGCKRVNTEFIISATVKAICGVY-NNM 58  
 DB 1 QDMITFQKHHTNRVDVCNIMSTNLF---HCKDKNTFYSPREPKAICGIIASKN 56  
 QY 59 VLSTTRQLNTRITRTSTTPRCPSTSTETNIVYCKENQVPYHFAIGRC 109  
 DB 57 VLTTSEFLSDC--NVTSRPCYKIKRSTNRCVTCENQAPVHFVGVGSC 104  
 RESULT 5  
 ANG3\_MOUSE STANDARD: PRT: 145 AA.  
 AC P97802;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DE 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Angiogenin-3 precursor (EC 3.1.27.-) (Angiogenin-related protein 2)  
 DE (EF-5).  
 GN ANG3 OR ANGL.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALE/c;  
 RX MEDLINE=97184476; PubMed=9032278;  
 RA Fu X., Kamps M.P.;  
 RT "Erga-Pbx1 induces aberrant expression of tissue-specific and developmentally regulated genes when expressed in NIH 3T3 fibroblasts.";  
 RL Mol. Cell. Biol. 17:1503-1512(1997).  
 CC -1- FUNCTION: ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY HYDROLYZING CELLULAR TRNAs (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: U72672; AAC05794.1;  
 DR HSSP: P10152; IAGL.  
 DR MGD: MGI:1201793; Angl.  
 DR InterPro: IPR001427; Rnasea.  
 DR Pfam: PF00074; rnaasea.1.  
 DR PRINTS: PR00794; RIBONUCLEASE.  
 DR ProDom: PD000535; Rnasea.1.  
 DR SMART: SM00092; Rnase\_Pc.1.  
 DR PROSITE: PS00127; Rnase\_Pancreatic.1.  
 KW Hydrolase; Nuclease; Endonuclease; Angiogenesis;  
 FT SIGNAL 1  
 FT CHAIN 25  
 FT MOD\_RES 25  
 FT ACT\_SITE 37  
 FT ACT\_SITE 64  
 FT ACT\_SITE 137  
 FT DISULFID 50  
 FT DISULFID 63  
 FT DISULFID 81  
 FT DISULFID 130  
 SQ SEQUENCE 145 AA; 16696 MW; DE9D3BC92F1D682C CRC64;

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Query Match Similarity 25.7%; Score 154.5; DB 1; Length 145;
Best Local Similarity 43.6%; Pred. No. 7,5e-10;
Matches 34; Conservative 12; Mismatches 22; Indels 9; Gaps 4;

OY 33 CKRVNFTFISSATYVKAIC-----TGVINNVLSTPRPLNCTRTSITPR-PCPYSSR 85
    ||||| : ||||| || | : ||||| ||| ||||| :
DB 63 CKRVNFTFHDHKKNNKAICGNGRPGV-NPRI-SNSRFQYTTCTHKGSPRPQYNAF 120
    : || : || : |||||
OY 86 TETNYVCYKCNQVPHF 103
    : || : || : |||||
DB 121 KDFRIVYIACEDGMPVHF 138

RESULT 6.
ID ANGR_MOUSE STANDARD: PRT: 145 AA.
AC 064438.
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 01-NOV-1997 (Rel. 35, Last annotation update)
DE Angiogenin-related protein precursor.
GN ANGRP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_Taxid:10090;
RN [1]
RF SEQUENCE FROM N.A.
RC STRAIN-129; TISSUE-Liver;
RX MEDLINE=96079109; PubMed=8530072;
RA Brown W.E., Noble V., Subramanian V., Shapiro R.;
RT "The mouse angiogenin gene family: structures of an angiogenin-related
RL protein gene and two pseudogenes.";
CC Genomics 29:200-206(1995).
CC -1 SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U25159; AAA91367.1; -
DR HSPB; P03950; 1A4Y.
DR MGD; MGI:104984; Angrp.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnasea; 1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR PRODOM; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal; Hydrolase; Nuclease; Endonuclease.
FT SIGNAL 1 24
FT CHAIN 25 145
FT MOD_RES 25 25
FT ACT_SITE 37 37
FT ACT_SITE 64 64
FT ACT_SITE 137 137
FT DISULFID 50 104
FT DISULFID 63 115
FT DISULFID 81 130
FT DISULFID 145 166
SO SEQUENCE 145 AA; 16612 MW; 22A6EB814429C4AD CXC64;

Query Match Similarity 24.8%; Score 149.5; DB 1; Length 145;
Best Local Similarity 43.4%; Pred. No. 2,6e-09;
Matches 33; Conservative 10; Mismatches 28; Indels 5; Gaps 3;

OY 33 CKRVNFTFISSATYVKAIC-----TGVINNVLSTPRPLNCTRTSITPR-PCPYSSR 87
    ||||| : ||||| || | : ||||| ||| ||||| :
DB 63 CKRVNFTFHDHKKNNKAICGKGSPPYGRNLEISRRQVYTTCTHKGRSPRPCCYRASKG 122
    : || : || : |||||

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OY      88  TNVICVKNCENOYPVHF 103
        || : || : ||||
DB      123  FRTIIGCENGMPVHF 138
        |||||

RESULT 7
RNP_BALAC
ID      RNP_BALAC      STANDARD:      PRT:      124 AA.
AC      P00673:
DT      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DT      15-JUN-2002 (Rel. 41, Last annotation update)
DE      Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
GN      RNASE1 OR RNS1.
OS      Balaenoptera acutorostrata (Minke whale) (lesser rorqual).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;
OC      Balaenopteridae; Balaenoptera.
OX      NCBI_TaxID=9767;
RN      [1]
RP      SEQUENCE.
RX      MEDLINE=76277855; PubMed=962870;
RA      Emlens M., Welling G.W., Beintema J.J.;
RT      "The amino acid sequence of pike-whale (lesser-rorqual) pancreatic
RT      ribonuclease.";
RL      Biochem. J. 157:317-323(1976).
CC      -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC      phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC      with 2',3'-cyclic phosphate intermediates.
CC      -1- SUBCELLULAR LOCATION: Secreted.
CC      -1- TISSUE SPECIFICITY: PANCREAS.
CC      -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
DR      PIR: A00818; NRMK.
DR      HSSP: P00656; ISRN.
DR      InterPro: IPR001427; RNaseA.
DR      Pfam: PF00074; RNaseA; 1.
DR      PRINTS: PR00794; RIBONUCLEASE.
DR      ProDom: PD000535; RNaseA; 1.
DR      SMART: SM00092; RNase_Pc; 1.
DR      PROSITE: PS00127; RNASE_PANCREATIC; 1.
KW      Hydrolase; Nuclease; Endonuclease; Glycoprotein.
FT      DISULFID 26 84
FT      DISULFID 40 95
FT      DISULFID 58 110
FT      DISULFID 65 72
FT      ACT_SITE 12 12
FT      ACT_SITE 41 41
FT      ACT_SITE 119 119
FT      CARBOHYD 76 76
FT      N-LINKED (GLCNAC. . .); IN 30% OF THE
FT      MOLECULES.
SQ      SEQUENCE 124 AA; 14125 MW; F57475459F657E20 CRC64;

Query Match 22.5%; Score 135.5; DB 1; Length 124;
Best Local Similarity 33.3%; Pred. No. 7.1e-08;
Matches 39; Conservative 16; Mismatches 39; Indels 23; Gaps 7;

OY      6  FQOKHII-----TPITICNTIMDNNNIYVGGCKRYNTFFISATYVKAICTGVIMNV 59
        |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB      8  FQRMHDSGNSFGNNPNVCNMNMRR-KMFGGRKRPNTGYNHELEEDYKAVCS---QKNV 63
        |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

OY      60  L-----STRFQNLNCTRTSTPRP-CPYSSRTETNYICVKE-NOY-PVHF 103
        ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB      64  LCKNGRTNCEYNSNSTMIHTDCRGTGSKSPYNCAYKTSQKEKHIIIVACEGNPYVPHF 120
        ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

RESULT 8
ANGI_MOUSE
ID      ANGI_MOUSE      STANDARD:      PRT:      145 AA.
AC      P21570:
DT      01-MAY-1991 (Rel. 18, Created)
DT      01-MAY-1991 (Rel. 18, Last sequence update)
DT      15-JUN-2002 (Rel. 41, Last annotation update)

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Db		123	FRRVIVACENGLPVHF	138
RESULT_9				
RNBR_BOVIN				
ID	RNBR_BOVIN	STANDARD:	PRT:	167 AA.
AC	P39873:			
DT	01-FEB-1995 (Rel. 31, Created)			
DT	01-FEB-1995 (Rel. 31, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Ribonuclease, brain precursor (EC 3.1.27.-) (BRB).			
GN	BRN.			
OS	Bos taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OX	Bovidae; Bos.			
OX	NCBI_TaxID=9913;			
RP	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=92093604; PubMed=1754384;			
RA	Sasso M.P., Carsana A., Confalone E., Cosi C., Sorrentino S.,			
RA	Viola M., Palmieri M., Russo E., Furia A.;			
RT	"Molecular cloning of the gene encoding the bovine brain ribonuclease			
RL	Nucleic Acids Res. 19:6469-6474(1991).			
RN	[2]			
RN	SEQUENCE OF 27-167, AND CARBOHYDRATE-LINKAGE SITES.			
RC	TISSUE=Brain;			
RX	MEDLINE=89214015; PubMed=3243767;			
RA	Watanabe H., Katch H., Ishii M., Komoda Y., Sanda A., Takizawa Y.,			
RA	Ohki K., Irie M.;			
RT	"Primary structure of a ribonuclease from bovine brain."			
RL	J. Biochem. 104:939-945(1988).			
RN	[3]			
RP	SEQUENCE OF 27-167 FROM N.A.			
RX	MEDLINE=96139017; PubMed=8587129;			
RA	Confalone E., Belmonte J.J., Sasso M.P., Carsana A., Palmieri M.,			
RA	Vento M.T., Furia A.;			
RT	"Molecular evolution of genes encoding ribonucleases in ruminant			
RT	species".			
RL	J. Mol. Evol. 41:850-858(1995).			
CC	-I- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.			
CC	-----			
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CC	entities requires a license agreement (See http://www.isb-sdb.ch/announce/			
CC	or send an email to license@isb-sdb.ch).			
CC	-----			
DR	EMBL; X59767; CAA42439.1; .			
DR	EMBL; S81744; AAB36138.1; .			
DR	PIR; S20066; S20066.			
DR	PIR; JX0056; JX0056.			
DR	HSSP; P0056; ZRNS.			
DR	GlycoSiteDB; P39873; .			
DR	InterPro; IPR001427; RNaseA.			
DR	pfam; PF00074; rnasea; 1.			
DR	PRINTS; PR00794; RIBONUCLEASE.			
DR	ProDom; PD000535; RNaseA; 1.			
DR	SMART; SM00092; RNase_PC; 1.			
DR	PROSITE; PS00127; RNASE_PANCREATIC; 1.			
KW	Hydroxylase; Nuclease; Endonuclease; Glycoprotein; Signal.			
FT	SIGNAL	1	26	
FT	CHAIN	27	167	RIBONUCLEASE, BRAIN.
FT	ACT_SITE	38	38	BY SIMILARITY.
FT	ACT_SITE	67	67	BY SIMILARITY.
FT	ACT_SITE	145	145	BY SIMILARITY.
FT	DISULFID	52	110	BY SIMILARITY.
FT	DISULFID	66	121	BY SIMILARITY.
FT	DISULFID	84	136	BY SIMILARITY.
FT	DISULFID	91	98	BY SIMILARITY.

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FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .)
FT FTID-CAR_000005.
FT CARBOHYD 155 155 O-LINKED.
FT CARBOHYD 159 159 O-LINKED.
FT CONFLICT 155 155 T -> S (IN REF. 2).
SQ SEQUENCE 167 AA; 18450 MW; 681CMA3C2FC459 CRC64;

Query Match
Best Local Similarity 22.8%; Score 133.5; DB 1; Length 167;
Matches 38; Conservative 17; Mismatches 43; Indels 23; Gaps 7;

QY 4 ATFOGKH-----INPILICNTIMDNIIYVGCGCKRVNFTFISSATYKAICTGVINM 57
D 32 AKFRROHMDSGSSSSSNPNVCNQMKNRR-RMTHGRCKRPVTFVHESLDVKAICS---QK 87
QY 58 NVL-----STRFOLNTCTRTSTTPRP-CPYSSRTETNYICVKE-NOY-PVHFA 104
D 88 NITCKNGHPNCYSKSTMTSDCRETGSSKYPNCAYKTSQKRYTVACGPNYPVPHF 147
QY 105 G 105
D 148 G 148

RESULT 10
RNP_PIG
ID RNP_PIG STANDARD; PRT; 124 AA.
AC P00671;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
GN RNAS1 OR RNS1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN (1)
RP SEQUENCE.
RX MEDLINE=70104197; PubMed=5460946;
RA Jackson R.L., Hirs C.H.W.;
RT "The primary structure of porcine pancreatic ribonuclease. II. The
RT amino acid sequence of the reduced S-aminoethylated protein.";
RL J. Biol. Chem. 245:637-653(1970).
RN (2)
RP REVISION TO 2.
RA Wierenga R.K., Huizinga J.D., Gaastera W., Welling G.W., Beintema J.J.;
RT "Affinity chromatography of porcine pancreatic ribonuclease and
RT reinvestigation of the N-terminal amino acid sequence.";
RL FEBS Lett. 31:181-185(1973).
RN (3)
RP DISULFIDE BONDS.
RX MEDLINE=70104198; PubMed=4904878;
RA Phelan J.U., Hirs C.H.W.;
RT "The primary structure of porcine pancreatic ribonuclease. 3. The
RT disulfide bonds.";
RL J. Biol. Chem. 245:654-661(1970).
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC with 2',3'-cyclic phosphate intermediates.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: PANCREAS.
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
DR HSSP; P00656; 1SRN.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR PRODOM; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Hydroxylase; Nuclease; Endonuclease; Glycoprotein.
FT DISULFID 26 84

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FT DISULFID 40 95
FT DISULFID 58 110
FT DISULFID 65 72
FT ACT_SITE 12 12
FT ACT_SITE 41 41
FT ACT_SITE 119 119
FT CARBOHYD 21 21
FT CARBOHYD 34 34
FT CARBOHYD 76 76
SQ SEQUENCE 124 AA; 13804 MW; 0AC28CDE1411845 CRC64;

Query Match
Best Local Similarity 22.0%; Score 132.5; DB 1; Length 124;
Matches 36; Conservative 19; Mismatches 42; Indels 17; Gaps 6;

QY 6 FOQKH-----INPILICNTIMDNIIYVGCGCKRVNFTFISSATYKAICTGV-INNM 58
D 8 FORQHMDDPSSSSSSNPNVCNQMKNRR-RMTHGRCKRPVTFVHESLDVKAICS---QK 66
QY 59 VLSSTRFOLNT-----CTRTSTTPRP-CPYSSRTETNYICVKE-NOY-PVHFA 103
D 67 NGQTCYQNSNSTPWHITDCROTSSKYPNCAYKASQKRIIIVACEGPNYPVPHF 120

RESULT 11
RNP_IGUG
ID RNP_IGUG STANDARD; PRT; 119 AA.
AC P80287;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
GN Iguana iguana (Common Iguana).
OS Iguana iguana (Common Iguana).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Iguaninae; Iguana.
OX NCBI_TaxID=6517;
RN (1)
RP SEQUENCE.
RX MEDLINE=94139745; PubMed=8307028;
RA Zhao W., Beintema J.J., Hofsteenge J.;
RT "The amino acid sequence of Iguana (Iguana Iguana) pancreatic
RT ribonuclease.";
RL Eur. J. Biochem. 219:641-646(1994).
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC with 2',3'-cyclic phosphate intermediates.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: PANCREAS.
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
DR HSSP; P00656; 1LSQ.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR PRODOM; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Hydroxylase; Nuclease; Endonuclease.
FT MOD_RES 1 1
FT DISULFID 25 80
FT DISULFID 39 91
FT DISULFID 57 106
FT ACT_SITE 10 10
FT ACT_SITE 40 40
FT ACT_SITE 113 113
SQ SEQUENCE 119 AA; 13324 MW; 6072F5B7B13BD5A CRC64;

Query Match
Best Local Similarity 21.8%; Score 131.5; DB 1; Length 119;
Matches 35; Conservative 16; Mismatches 51; Indels 13; Gaps 4;

QY 1 QMAATFOQKH-----INPILICNTIMDNIIYVGCGCKRVNFTFISSATYKAICTGV-INNM 51

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RX MEDLINE-96139017; PubMed-8587129;
RA Confalone E., Belmonte J.J., Sasso M.P., Carsana A., Palmieri M.,
RA Vento M.T., Furia A.;
RT "Molecular evolution of genes encoding ribonucleases in ruminant
RL species."
RL J. Mol. Evol. 41:850-858(1995).
RN
RP (2)
RP SEQUENCE OF 31-114 FROM N.A.
RX MEDLINE-93367815; PubMed-8360916;
RA Breukelman H.J., Belmonte J.J., Confalone E., Costanzo C., Sasso M.P.,
RA Carsana A., Palmieri M., Furia A.;
RT "Sequences related to the ox pancreatic ribonuclease coding region in
RL the genomic DNA of mammalian species."
RL J. Mol. Evol. 37:29-35(1993).
CC
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
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CC
DR EMBL: S81743; AAB36137.1; -
DR EMBL: S65126; AAB27931.1; -
DR HSSP: P00656; 2RNS.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA.1.
DR PRINTS: PR00794; RIBONUCLEASE.
DR ProDom: PD000535; RNaseA.1.
DR SMART: SM00092; RNaseA.1.
DR PROSITE: PS00127; RNase_PANCREATIC.1.
KW Hydrolyase; Nuclease; Endonuclease; Glycoprotein.
FT ACT_SITE 41
FT DISULFID 26 84 BY SIMILARITY.
FT DISULFID 40 95 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT DISULFID 65 72 BY SIMILARITY.
FT CARBOHYD 129 129 N-LINKED (GLCNAC...) (BY SIMILARITY).
FT CARBOHYD 129 129 O-LINKED (BY SIMILARITY).
SQ SEQUENCE 141 AA; 15592 MM; 73745EP9079591F CRC64;

Query Match 21.2%; Score 127.5; DB 1; Length 141;
Best Local Similarity 30.6%; Pred. No. 5.9e-07;
Matches 37; Conservative 17; Mismatches 44; Indels 23; Gaps 7;

OY 4 ATFOOKHI-----INTPLICNTIMDNNTIYVGGCKRNTFLISSATTVAKICGVIM 57
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 6 AKFRROHMDGSSSSNSNVCNOMMKRR-RMTHGRCKPNTFVHESLADVKAACS---OK 61
OY 58 NVL-----STTRFOLNCTRTSTIPRP-CPYSSRTETNYICVKE-NQY-PVHFA 104
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 62 NITCKNGOPNCVQNSNTMNTDCRETGSSKYPNCAYKTSQOKYITVACEGNPVVPHD 121
OY 105 G 105
DB 122 G 122

RESULT 15
RNRB_AXIPR STANDARD: PRT: 151 AA.
AC P87350;
DT 15-DEC-1998 (Rel. 37, created)
DT 15-DEC-1998 (Rel. 37, last sequence update)
DT 16-OCT-2001 (Rel. 40, last annotation update)
DE Ribonuclease, brain (EC 3.1.27.-) (BRB).
GN BRN.
OS Axis porcinus (Hog deer).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
OC Cervidae; Cervinae; Axis.

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OX NCBI_TaxID=57737;
RN (1)
RN SEQUENCE FROM N.A.
RX MEDLINE-98278842; PubMed-9611269;
RA Breukelman H.J., van der Munnik N., Kleinedam R.G., Furia A.,
RA Belmonte J.J.;
RT "Secretory ribonuclease genes and pseudogenes in true ruminants."
RL Gene 212:259-268(1998).
CC
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
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CC
DR EMBL: Y11670; CAA72368.1; -
DR HSSP: P00656; ISRN.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA.1.
DR PRINTS: PR00794; RIBONUCLEASE.
DR ProDom: PD000535; RNaseA.1.
DR SMART: SM00092; RNaseA.1.
DR PROSITE: PS00127; RNase_PANCREATIC.1.
KW Hydrolyase; Nuclease; Endonuclease; Glycoprotein.
FT ACT_SITE 41
FT DISULFID 26 84 BY SIMILARITY.
FT DISULFID 40 95 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT DISULFID 65 72 BY SIMILARITY.
FT CARBOHYD 129 129 N-LINKED (GLCNAC...) (BY SIMILARITY).
FT CARBOHYD 133 133 O-LINKED (BY SIMILARITY).
SQ SEQUENCE 151 AA; 16819 MM; E95F3757FC5B233 CRC64;

Query Match 21.2%; Score 127.5; DB 1; Length 151;
Best Local Similarity 30.6%; Pred. No. 6.4e-07;
Matches 37; Conservative 17; Mismatches 44; Indels 23; Gaps 7;

OY 4 ATFOOKHI-----INTPLICNTIMDNNTIYVGGCKRNTFLISSATTVAKICGVIM 57
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 6 AKFRROHMDGSSSSNSNVCNOMMKRR-RMTHGRCKPNTFVHESLADVKAACS---OK 61
OY 58 NVL-----STTRFOLNCTRTSTIPRP-CPYSSRTETNYICVKE-NQY-PVHFA 104
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 62 NITCKNGOPNCVQNSNTMNTDCRETGSSKYPNCAYKTSQOKYITVACEGNPVVPHD 121
OY 105 G 105
DB 122 G 122

Search completed: June 25, 2003, 14:50:05
Job time : 5.71318 secs

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